Jeremy P Cheadle

List of Publications by Year
in descending order

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63 papers	7,979 citations	109321 35 h-index	144013 57 g-index
64 all docs	64 docs citations	64 times ranked	9308 citing authors

#	Article	IF	Citations
1	Genetic variation in ST6GAL1 is a determinant of capecitabine and oxaliplatin induced handâ€foot syndrome. International Journal of Cancer, 2022, , .	5.1	3
2	Germline MBD4 deficiency causes a multi-tumor predisposition syndrome. American Journal of Human Genetics, 2022, 109, 953-960.	6.2	23
3	Lack of an association between gallstone disease and bilirubin levels with risk of colorectal cancer: a Mendelian randomisation analysis. British Journal of Cancer, 2021, 124, 1169-1174.	6.4	6
4	Genomeâ€wide association studies of toxicity to oxaliplatin and fluoropyrimidine chemotherapy with or without cetuximab in 1800 patients with advanced colorectal cancer. International Journal of Cancer, 2021, 149, 1713-1722.	5.1	7
5	A genome-wide search for determinants of survival in 1926 patients with advanced colorectal cancer with follow-up in over 22,000 patients. European Journal of Cancer, 2021, 159, 247-258.	2.8	6
6	Modifiable pathways for colorectal cancer: a mendelian randomisation analysis. The Lancet Gastroenterology and Hepatology, 2020, 5, 55-62.	8.1	79
7	Comprehensive analysis of colorectal cancer-risk loci and survival outcome: A prognostic role for CDH1 variants. European Journal of Cancer, 2020, 124, 56-63.	2.8	10
8	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	12.8	172
9	Pattern Recognition Receptor Polymorphisms as Predictors of Oxaliplatin Benefit in Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 828-836.	6.3	10
10	Genomeâ€wide association study and metaâ€analysis in Northern European populations replicate multiple colorectal cancer risk loci. International Journal of Cancer, 2018, 142, 540-546.	5.1	26
11	Role for Nucleotide Excision Repair Gene Variants in Oxaliplatin-Induced Peripheral Neuropathy. JCO Precision Oncology, 2018, 2, 1-18.	3.0	1
12	Pharmacogenetic analyses of 2183 patients with advanced colorectal cancer; potential role for common dihydropyrimidine dehydrogenase variants in toxicity to chemotherapy. European Journal of Cancer, 2018, 102, 31-39.	2.8	25
13	Comprehensive pharmacogenetic profiling of the epidermal growth factor receptor pathway for biomarkers of response to, and toxicity from, cetuximab. Journal of Medical Genetics, 2017, 54, 567-571.	3.2	4
14	Mendelian randomisation implicates hyperlipidaemia as a risk factor for colorectal cancer. International Journal of Cancer, 2017, 140, 2701-2708.	5.1	76
15	Pro-inflammatory fatty acid profile and colorectal cancer risk: A Mendelian randomisation analysis. European Journal of Cancer, 2017, 84, 228-238.	2.8	81
16	BRAF and NRAS Locus-Specific Variants Have Different Outcomes on Survival to Colorectal Cancer. Clinical Cancer Research, 2017, 23, 2742-2749.	7.0	32
17	Mendelian randomisation analysis strongly implicates adiposity with risk of developing colorectal cancer. British Journal of Cancer, 2016, 115, 266-272.	6.4	57
18	Variation at 2q35 (PNKDandTMBIM1) influences colorectal cancer risk and identifies a pleiotropic effect with inflammatory bowel disease. Human Molecular Genetics, 2016, 25, 2349-2359.	2.9	37

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19	Common genetic variation and survival after colorectal cancer diagnosis: a genome-wide analysis. Carcinogenesis, 2016, 37, 87-95.	2.8	62
20	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. Scientific Reports, 2015, 5, 17369.	3.3	35
21	A new GWAS and meta-analysis with 1000Genomes imputation identifies novel risk variants for colorectal cancer. Scientific Reports, 2015, 5, 10442.	3.3	109
22	Analyses of 7,635 Patients with Colorectal Cancer Using Independent Training and Validation Cohorts Show That rs9929218 in CDH1 Is a Prognostic Marker of Survival. Clinical Cancer Research, 2015, 21, 3453-3461.	7.0	24
23	MUTYH-Associated Colorectal Polyposis. , 2015, , 2969-2973.		0
24	MUTYH-Associated Colorectal Polyposis. , 2015, , 1-4.		0
25	Response. Journal of the National Cancer Institute, 2014, 106, .	6.3	0
26	Mismatch Repair Status and BRAF Mutation Status in Metastatic Colorectal Cancer Patients: A Pooled Analysis of the CAIRO, CAIRO2, COIN, and FOCUS Studies. Clinical Cancer Research, 2014, 20, 5322-5330.	7.0	561
27	Role of the Oxidative DNA Damage Repair Gene OGG1 in Colorectal Tumorigenesis. Journal of the National Cancer Institute, 2013, 105, 1249-1253.	6.3	22
28	Exome Resequencing Identifies Potential Tumor-Suppressor Genes that Predispose to Colorectal Cancer. Human Mutation, 2013, 34, 1026-1034.	2.5	48
29	Somatic Profiling of the Epidermal Growth Factor Receptor Pathway in Tumors from Patients with Advanced Colorectal Cancer Treated with Chemotherapy Â± Cetuximab. Clinical Cancer Research, 2013, 19, 4104-4113.	7.0	95
30	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	21.4	210
31	Addition of cetuximab to oxaliplatin-based first-line combination chemotherapy for treatment of advanced colorectal cancer: results of the randomised phase 3 MRC COIN trial. Lancet, The, 2011, 377, 2103-2114.	13.7	876
32	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. PLoS Genetics, 2011, 7, e1002105.	3.5	188
33	MUTYH-Associated Colorectal Polyposis. , 2011, , 2420-2423.		0
34	Meta-analysis of three genome-wide association studies identifies susceptibility loci for colorectal cancer at 1q41, 3q26.2, 12q13.13 and 20q13.33. Nature Genetics, 2010, 42, 973-977.	21.4	335
35	MUTYH-Associated Polyposis. , 2010, , 133-146.		0
36	MUTYH-associated polyposisâ€"From defect in base excision repair to clinical genetic testing. DNA Repair, 2007, 6, 274-279.	2.8	135

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37	Rapid recognition of aberrant dHPLC elution profiles using the Transgenomic NavigatorTM software. Human Mutation, 2005, 26, 165-165.	2.5	5
38	A mouse model of tuberous sclerosis 1 showing background specific early post-natal mortality and metastatic renal cell carcinoma. Human Molecular Genetics, 2005, 14, 1839-1850.	2.9	63
39	Functional characterization of two human MutY homolog (hMYH) missense mutations (R227W and) Tj ETQq1 1 0.784314 rgBT /Over Nucleic Acids Research, 2005, 33, 597-604.	14.5	61
40	Inherited variants in MYH are unlikely to contribute to the risk of lung carcinoma. Human Genetics, 2004, 114, 207-210.	3.8	39
41	Comprehensive analysis of the contribution of germlineMYH variation to early-onset colorectal cancer. International Journal of Cancer, 2004, 109, 554-558.	5.1	114
42	Characterizing mutations in samples with low-level mosaicism by collection and analysis of DHPLC fractionated heteroduplexes. Human Mutation, 2003, 21, 112-115.	2.5	43
43	Autosomal recessive colorectal adenomatous polyposis due to inherited mutations of MYH. Lancet, The, 2003, 362, 39-41.	13.7	421
44	Exposing the MYtH about base excision repair and human inherited disease. Human Molecular Genetics, 2003, 12, R159-R165.	2.9	80
45	Biallelic germline mutations in MYH predispose to multiple colorectal adenoma and somatic G:C->T:A mutations. Human Molecular Genetics, 2002, 11, 2961-2967.	2.9	365
46	Temperature modulation of DHPLC analysis for detection of coexisting constitutional and mosaic sequence variants in TSC2. Journal of Proteomics, 2002, 51, 161-164.	2.4	15
47	Inherited variants of MYH associated with somatic G:Câ†'T:A mutations in colorectal tumors. Nature Genetics, 2002, 30, 227-232.	21.4	1,239
48	Different combinations of biallelic APC mutation confer different growth advantages in colorectal tumours. Cancer Research, 2002, 62, 363-6.	0.9	32
49	LD-PCR coupled to long-read direct sequencing: an approach for mutation detection in genes with compact genomic structures. Journal of Proteomics, 2001, 47, 131-136.	2.4	0
50	Low level mosaicism detectable by DHPLC but not by direct sequencing. Human Mutation, 2001, 17, 233-234.	2.5	53
51	The tuberous sclerosis-1 (TSC1) gene product hamartin suppresses cell growth and augments the expression of the TSC2 product tuberin by inhibiting its ubiquitination. Oncogene, 2000, 19, 6306-6316.	5.9	227
52	Genomic organization and comparative analysis of the mouse tuberous sclerosis 1 (Tsc1) locus. Mammalian Genome, 2000, 11, 1135-1138.	2.2	5
53	Molecular genetic advances in tuberous sclerosis. Human Genetics, 2000, 107, 97-114.	3.8	323
54	Molecular analysis of the TSC1 and TSC2 tumour suppressor genes in sporadic glial and glioneuronal tumours. Human Genetics, 2000, 107, 350-356.	3.8	41

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55	Germline APC variants in patients with multiple colorectal adenomas, with evidence for the particular importance of E1317Q. Human Molecular Genetics, 2000, 9, 2215-2221.	2.9	125
56	Application and evaluation of denaturing HPLC for molecular genetic analysis in tuberous sclerosis. Human Genetics, 2000, 106, 663-668.	3.8	58
57	Application and evaluation of denaturing HPLC for molecular genetic analysis in tuberous sclerosis. Human Genetics, 2000, 106, 663-668.	3.8	15
58	Comprehensive Mutation Analysis of TSC1 and TSC2â€"and Phenotypic Correlations in 150 Families with Tuberous Sclerosis. American Journal of Human Genetics, 1999, 64, 1305-1315.	6.2	453
59	Identification of a leader exon and a core promoter for the rat tuberous sclerosis 2 (Tsc2) gene and structural comparison with the human homolog. Mammalian Genome, 1997, 8, 554-558.	2.2	30
60	Comparative Analysis and Genomic Structure of the Tuberous Sclerosis 2 (TSC2) Gene in Human and Pufferfish. Human Molecular Genetics, 1996, 5, 131-137.	2.9	66
61	Cystic fibrosis mutation analysis: Report from 22 U.K. regional genetics laboratories. Human Mutation, 1995, 6, 326-333.	2.5	38
62	Relationship between trinucleotide repeat expansion and phenotypic variation in Huntington's disease. Nature Genetics, 1993, 4, 393-397.	21.4	672
63	Direct sequencing of the complete CFTR gene: the molecular characterisation of 99.5% of CF chromosomes in Wales. Human Molecular Genetics, 1993, 2, 1551-1556.	2.9	41